

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(I) APPLICANTS: Ken Stokes
Josée Morissette

(ii) TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATMENT

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and Norris
(B) STREET: One Liberty Place - 46th Floor
(C) CITY: Philadelphia
(D) STATE: PA
(E) COUNTRY: U.S.A.
(F) ZIP: 19103

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WordPerfect 6.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: N/A
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Paul K. Legaard
(B) REGISTRATION NUMBER: 38,534
(C) REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(I) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6048 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GCA AAC TTC CTA TTA CCT CGG GGC ACC ACC AGC AGC TTC CGC AGG 45
Met Ala Asn Phe Leu Leu Pro Arg Gly Thr Ser Ser Phe Arg Arg
1 5 10 15

TTC ACA CGG GAG TCC CTG GCA GCC ATC GAG AAG CGC ATG GCG GAG 90
Phe Thr Arg Glu Ser Leu Ala Ala Ile Glu Lys Arg Met Ala Glu

20	25	30	
AAG CAA GCC CGC GGC TCA ACC ACC TTG CAG GAG AGC CGA GAG GGG Lys Gln Ala Arg Gly Ser Thr Thr Leu Gln Glu Ser Arg Glu Gly 35	40	45	135
CTG CCC GAG GAG GAG GCT CCC CGG CCC CAG CTG GAC CTG CAG GCC Leu Pro Glu Glu Ala Pro Arg Pro Gln Leu Asp Leu Gln Ala 50	55	60	180
TCC AAA AAG CTG CCA GAT CTC TAT GGC AAT CCA CCC CAA GAG CTC Ser Lys Lys Leu Pro Asp Leu Tyr Gly Asn Pro Pro Gln Glu Leu 65	70	75	225
ATC GGA GAG CCC CTG GAG GAC CTG GAC CCC TTC TAT AGC ACC CAA Ile Gly Glu Pro Leu Glu Asp Leu Asp Pro Phe Tyr Ser Thr Gln 80	85	90	270
AAG ACT TTC ATC GTA CTG AAT AAA GGC AAG ACC ATC TTC CGG TTC Lys Thr Phe Ile Val Leu Asn Lys Gly Lys Thr Ile Phe Arg Phe 95	100	105	315
AGT GCC ACC AAC GCC TTG TAT GTC CTC AGT CCC TTC CAC CCA GTT Ser Ala Thr Asn Ala Leu Tyr Val Leu Ser Pro Phe His Pro Val 110	115	120	360
CGG AGA GCG GCT GTG AAG ATT CTG GTT CAC TCG CTC TTC AAC ATG Arg Arg Ala Ala Val Lys Ile Leu Val His Ser Leu Phe Asn Met 125	130	135	405
CTC ATC ATG TGC ACC ATC CTC ACC AAC TGC GTG TTC ATG GCC CAG Leu Ile Met Cys Thr Ile Leu Thr Asn Cys Val Phe Met Ala Gln 140	145	150	450
CAC GAC CCT CCA CCC TGG ACC AAG TAT GTC GAG TAC ACC TTC ACC His Asp Pro Pro Pro Trp Thr Lys Tyr Val Glu Tyr Thr Phe Thr 155	160	165	495
GCC ATT TAC ACC TTT GAG TCT CTG GTC AAG ATT CTG GCT CGA GCT Ala Ile Tyr Thr Phe Glu Ser Leu Val Lys Ile Leu Ala Arg Ala 170	175	180	540
TTC TGC CTG CAC GCG TTC ACT TTC CTT CGG GAC CCA TGG AAC TGG Phe Cys Leu His Ala Phe Thr Phe Leu Arg Asp Pro Trp Asn Trp 185	190	195	585
CTG GAC TTT AGT GTG ATT ATC ATG GCA TAC ACA ACT GAA TTT GTG Leu Asp Phe Ser Val Ile Ile Met Ala Tyr Thr Thr Glu Phe Val 200	205	210	630
GAC CTG GGC AAT GTC TCA GCC TTA CGC ACC TTC CGA GTC CTC CGG Asp Leu Gly Asn Val Ser Ala Leu Arg Thr Phe Arg Val Leu Arg 215	220	225	675
GCC CTG AAA ACT ATA TCA GTC ATT TCA GGG CTG AAG ACC ATC GTG Ala Leu Lys Thr Ile Ser Val Ile Ser Gly Leu Lys Thr Ile Val			720

230	235	240	
GGG GCC CTG ATC CAG TCT GTG AAG AAG CTG GCT GAT GTG ATG GTC Gly Ala Leu Ile Gln Ser Val Lys Lys Leu Ala Asp Val Met Val 245	250	255	765
CTC ACA GTC TTC TGC CTC AGC GTC TTT GCC CTC ATC GGC CTG CAG Leu Thr Val Phe Cys Leu Ser Val Phe Ala Leu Ile Gly Leu Gln 260	265	270	810
CTC TTC ATG GGC AAC CTA AGG CAC AAG TGT GTG CGC AAC TTC ACA Leu Phe Met Gly Asn Leu Arg His Lys Cys Val Arg Asn Phe Thr 275	280	285	855
GCG CTC AAC GGC ACC AAC GGC TCC GTG GAG GCC GAC GGC TTG GTC Ala Leu Asn Gly Thr Asn Gly Ser Val Glu Ala Asp Gly Leu Val 290	295	300	900
TGG GAA TCC CTG GAC CTT TAC CTC AGT GAT CCA GAA AAT TAC CTG Trp Glu Ser Leu Asp Leu Tyr Leu Ser Asp Pro Glu Asn Tyr Leu 305	310	315	945
CTC AAG AAC GGC ACC TCT GAT GTG TTA CTG TGT GGG AAC AGC TCT Leu Lys Asn Gly Thr Ser Asp Val Leu Leu Cys Gly Asn Ser Ser 320	325	330	990
GAC GCT GGG ACA TGT CCG GAG GGC TAC CGG TGC CTA AAG GCA GGC Asp Ala Gly Thr Cys Pro Glu Gly Tyr Arg Cys Leu Lys Ala Gly 335	340	345	1035
GAG AAC CCC GAC CAC GGC TAC ACC AGC TTC GAT TCC TTT GCC TGG Glu Asn Pro Asp His Gly Tyr Thr Ser Phe Asp Ser Phe Ala Trp 350	355	360	1080
GCC TTT CTT GCA CTC TTC CGC CTG ATG ACG CAG GAC TGC TGG GAG Ala Phe Leu Ala Leu Phe Arg Leu Met Thr Gln Asp Cys Trp Glu 365	370	375	1125
CGC CTC TAT CAG CAG ACC CTC AGG TCC GCA GGG AAG ATC TAC ATG Arg Leu Tyr Gln Gln Thr Leu Arg Ser Ala Gly Lys Ile Tyr Met 380	385	390	1170
ATC TTC TTC ATG CTT GTC ATC TTC CTG GGG TCC TTC TAC CTG GTG Ile Phe Phe Met Leu Val Ile Phe Leu Gly Ser Phe Tyr Leu Val 395	400	405	1215
AAC CTG ATC CTG GCC GTG GTC GCA ATG GCC TAT GAG GAG CAA AAC Asn Leu Ile Leu Ala Val Val Ala Met Ala Tyr Glu Glu Gln Asn 410	415	420	1260
CAA GCC ACC ATC GCT GAG ACC GAG GAG AAG GAA AAG CGC TTC CAG Gln Ala Thr Ile Ala Glu Thr Glu Glu Lys Glu Lys Arg Phe Gln 425	430	435	1305
GAG GCC ATG GAA ATG CTC AAG AAA GAA CAC GAG GCC CTC ACC ATC Glu Ala Met Glu Met Leu Lys Lys Glu His Glu Ala Leu Thr Ile			1350

440	445	450	
AGG GGT GTG GAT ACC GTG TCC CGT AGC TCC TTG GAG ATG TCC CCT Arg Gly Val Asp Thr Val Ser Arg Ser Ser Leu Glu Met Ser Pro			1395
455	460	465	
TTG GCC CCA GTA AAC AGC CAT GAG AGA AGA AGC AAG AGG AGA AAA Leu Ala Pro Val Asn Ser His Glu Arg Arg Ser Lys Arg Arg Lys			1440
470	475	480	
CGG ATG TCT TCA GGA ACT GAG GAG TGT GGG GAG GAC AGG CTC CCC Arg Met Ser Ser Gly Thr Glu Glu Cys Gly Glu Asp Arg Leu Pro			1485
485	490	495	
AAG TCT GAC TCA GAA GAT GGT CCC AGA GCA ATG AAT CAT CTC AGC Lys Ser Asp Ser Glu Asp Gly Pro Arg Ala Met Asn His Leu Ser			1520
500	505	510	
CTC ACC CGT GGC CTC AGC AGG ACT TCT ATG AAG CCA CGT TCC AGC Leu Thr Arg Gly Leu Ser Arg Thr Ser Met Lys Pro Arg Ser Ser			1565
515	520	525	
CGC GGG AGC ATT TTC ACC TTT CGC AGG CGA GAC CTG GGT TCT GAA Arg Gly Ser Ile Phe Thr Phe Arg Arg Arg Asp Leu Gly Ser Glu			1620
530	535	540	
GCA GAT TTT GCA GAT GAT GAA AAC AGC ACA GCG CGG GAG AGC GAG Ala Asp Phe Ala Asp Asp Glu Asn Ser Thr Ala Arg Glu Ser Glu			1665
545	550	555	
AGC CAC CAC ACA TCA CTG CTG GTG CCC TGG CCC CTG CGC CGG ACC Ser His His Thr Ser Leu Leu Val Pro Trp Pro Leu Arg Arg Thr			1710
560	565	570	
AGT GCC CAG GGA CAG CCC AGT CCC GGA ACC TCG GCT CCT GGC CAC Ser Ala Gln Gly Gln Pro Ser Pro Gly Thr Ser Ala Pro Gly His			1755
575	580	585	
GCC CTC CAT GGC AAA AAG AAC AGC ACT GTG GAC TGC AAT GGG GTG Ala Leu His Gly Lys Lys Asn Ser Thr Val Asp Cys Asn Gly Val			1800
590	595	600	
GTC TCA TTA CTG GGG GCA GGC GAC CCA GAG GCC ACA TCC CCA GGA Val Ser Leu Leu Gly Ala Gly Asp Pro Glu Ala Thr Ser Pro Gly			1845
605	610	615	
AGC CAC CTC CTC CGC CCT GTG ATG CTA GAG CAC CCG CCA GAC ACG Ser His Leu Leu Arg Pro Val Met Leu Glu His Pro Pro Asp Thr			1890
620	625	630	
ACC ACG CCA TCG GAG GAG CCA GGC GGC CCC CAG ATG CTG ACC TCC Thr Thr Pro Ser Glu Glu Pro Gly Gly Pro Gln Met Leu Thr Ser			1935
635	640	645	
CAG GCT CCG TGT GTA GAT GGC TTC GAG GAG CCA GGA GCA CGG CAG Gln Ala Pro Cys Val Asp Gly Phe Glu Glu Pro Gly Ala Arg Gln			1980

650	655	660	
CGG GCC CTC AGC GCA GTC AGC GTC CTC ACA AGC GCA CTG GAA GAG Arg Ala Leu Ser Ala Val Ser Val Leu Thr Ser Ala Leu Glu Glu			2025
665	670	675	
TTA GAG GAG TCT CGC CAC AAG TGT CCA CCA TGC TGG AAC CGT CTC Leu Glu Glu Ser Arg His Lys Cys Pro Pro Cys Trp Asn Arg Leu			2070
680	685	690	
GCC CAG CGC TAC CTG ATC TGG GAG TGC TGC CCG CTG TGG ATG TCC Ala Gln Arg Tyr Leu Ile Trp Glu Cys Cys Pro Leu Trp Met Ser			2115
695	700	705	
ATC AAG CAG GGA GTG AAG TTG GTG GTC ATG GAC CCG TTT ACT GAC Ile Lys Gln Gly Val Lys Leu Val Val Met Asp Pro Phe Thr Asp			2160
710	715	720	
CTC ACC ATC ACT ATG TGC ATC GTA CTC AAC ACA CTC TTC ATG GCG Leu Thr Ile Thr Met Cys Ile Val Leu Asn Thr Leu Phe Met Ala			2205
725	730	735	
CTG GAG CAC TAC AAC ATG ACA AGT GAA TTC GAG GAG ATG CTG CAG Leu Glu His Tyr Asn Met Thr Ser Glu Phe Glu Glu Met Leu Gln			2250
740	745	750	
GTC GGA AAC CTG GTC TTC ACA GGG ATT TTC ACA GCA GAG ATG ACC Val Gly Asn Leu Val Phe Thr Gly Ile Phe Thr Ala Glu Met Thr			2295
755	760	765	
TTC AAG ATC ATT GCC CTC GAC CCC TAC TAC TTC CAA CAG GGC Phe Lys Ile Ile Ala Leu Asp Pro Tyr Tyr Phe Gln Gln Gly			2340
770	775	780	
TGG AAC ATC TTC GAC AGC ATC ATC GTC ATC CTT AGC CTC ATG GAG Trp Asn Ile Phe Asp Ser Ile Ile Val Ile Leu Ser Leu Met Glu			2385
785	790	795	
CTG GGC CTG TCC CGC ATG AGC AAC TTG TCG GTG CTG CGC TCC TTC Leu Gly Leu Ser Arg Met Ser Asn Leu Ser Val Leu Arg Ser Phe			2430
800	805	810	
CGC CTG CTG CGG GTC TTC AAG CTG GCC AAA TCA TGG CCC ACC CTG Arg Leu Leu Arg Val Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu			2475
815	820	825	
AAC ACA CTC ATC AAG ATC ATC GGG AAC TCA GTG GGG GCA CTG GGG Asn Thr Leu Ile Lys Ile Ile Gly Asn Ser Val Gly Ala Leu Gly			2520
830	835	840	
AAC CTG ACA CTG GTG CTA GCC ATC ATC GTG TTC ATC TTT GCT GTG Asn Leu Thr Leu Val Leu Ala Ile Ile Val Phe Ile Phe Ala Val			2565
845	850	855	
GTG GGC ATG CAG CTC TTT GGC AAG AAC TAC TCG GAG CTG AGG GAC Val Gly Met Gln Leu Phe Gly Lys Asn Tyr Ser Glu Leu Arg Asp			2610

860	865	870	
AGC GAC TCA GGC CTG CTG CCT CGC TGG CAC ATG ATG GAC TTC TTT Ser Asp Ser Gly Leu Leu Pro Arg Trp His Met Met Asp Phe Phe 875	880	885	2655
CAT GCC TTC CTA ATC ATC TTC CGC ATC CTC TGT GGA GAG TGG ATC His Ala Phe Leu Ile Ile Phe Arg Ile Leu Cys Gly Glu Trp Ile 890	895	900	2700
GAG ACC ATG TGG GAC TGC ATG GAG GTG TCG GGG CAG TCA TTA TGC Glu Thr Met Trp Asp Cys Met Glu Val Ser Gly Gln Ser Leu Cys 905	910	915	2745
CTG CTG GTC TTC TTG CTT GTT ATG GTC ATT GGC AAC CTT GTG GTC Leu Leu Val Phe Leu Leu Val Met Val Ile Gly Asn Leu Val Val 920	925	930	2790
CTG AAT CTC TTC CTG GCC TTG CTG CTC AGC TCC TTC AGT GCA GAC Leu Asn Leu Phe Leu Ala Leu Leu Ser Ser Phe Ser Ala Asp 935	940	945	2835
AAC CTC ACA GCC CCT GAT GAG GAC AGA GAG ATG AAC AAC CTC CAG Asn Leu Thr Ala Pro Asp Glu Asp Arg Glu Met Asn Asn Leu Gln 950	955	960	2880
CTG GCC CTG GCC CGC ATC CAG AGG GGC CTG CGC TTT GTC AAG CGG Leu Ala Leu Ala Arg Ile Gln Arg Gly Leu Arg Phe Val Lys Arg 965	970	975	2925
ACC ACC TGG GAT TTC TGC TGT GGT CTC CTG CGG CAC CGG CCT CAG Thr Thr Trp Asp Phe Cys Cys Gly Leu Arg His Arg Pro Gln 980	985	990	2970
AAG CCC GCA GCC CTT GCC GCC CAG GGC CAG CTG CCC AGC TGC ATT Lys Pro Ala Ala Leu Ala Ala Gln Gly Gln Leu Pro Ser Cys Ile 995	1000	1005	3015
GCC ACC CCC TAC TCC CCG CCA CCC CCA GAG ACG GAG AAG GTG CCT Ala Thr Pro Tyr Ser Pro Pro Pro Glu Thr Glu Lys Val Pro 1010	1015	1020	3060
CCC ACC CGC AAG GAA ACA CAG TTT GAG GAA GGC GAG CAA CCA GGC Pro Thr Arg Lys Glu Thr Gln Phe Glu Glu Gly Glu Gln Pro Gly 1025	1030	1035	3105
CAG GGC ACC CCC GGG GAT CCA GAC GCC GTG TGT GTG CCC ATC GCT Gln Gly Thr Pro Gly Asp Pro Glu Pro Val Cys Val Pro Ile Ala 1040	1045	1050	3150
GTG GCC GAG TCA GAC ACA GAT GAC CAA GAA GAG GAT GAG GAG AAC Val Ala Glu Ser Asp Thr Asp Asp Gln Glu Glu Asp Glu Glu Asn 1055	1060	1065	3195
AGC CTG GGC ACG GAG GAG TCC AGC AAG CAG CAG GAA TCC CAG			3240

Ser Leu Gly Thr Glu Glu Glu Ser Ser Lys Gln Gln Glu Ser Gln
1070 1075 1080

CCT GTG TCC GGC TGG CCC AGA GGC CCT CCG GAT TCC AGG ACC TGG 3285
Pro Val Ser Gly Trp Pro Arg Gly Pro Pro Asp Ser Arg Thr Trp
1085 1090 1095

AGC CAG GTG TCA GCG ACT GCC TCC TCT GAG GCC GAG GCC AGT GCA 3330
Ser Gln Val Ser Ala Thr Ala Ser Ser Glu Ala Glu Ala Ser Ala
1100 1105 1110

TCT CAG GCC GAC TGG CGG CAG CAG TGG AAA GCG GAA CCC CAG GCC 3375
Ser Gln Ala Asp Trp Arg Gln Gln Trp Lys Ala Glu Pro Gln Ala
1115 1120 1125

CCA GGG TGC GGT GAG ACC CCA GAG GAC AGT TGC TCC GAG GGC AGC 3420
Pro Gly Cys Gly Glu Thr Pro Glu Asp Ser Cys Ser Glu Gly Ser
1130 1135 1140

ACA GCA GAC ATG ACC AAC ACC GCT GAG CTC CTG GAG CAG ATC CCT 3465
Thr Ala Asp Met Thr Asn Thr Ala Glu Leu Leu Glu Gln Ile Pro
1145 1150 1155

GAC CTC GGC CAG GAT GTC AAG GAC CCA GAG GAC TGC TTC ACT GAA 3510
Asp Leu Gly Gln Asp Val Lys Asp Pro Glu Asp Cys Phe Thr Glu
1160 1165 1170

GGC TGT GTC CGG CGC TGT CCC TGC TGT GCG GTG GAC ACC ACA CAG 3555
Gly Cys Val Arg Arg Cys Pro Cys Cys Ala Val Asp Thr Thr Gln
1175 1180 1185

GCC CCA GGG AAG GTC TGG TGG CGG TTG CGC AAG ACC TGC TAC CAC 3600
Ala Pro Gly Lys Val Trp Trp Arg Leu Arg Lys Thr Cys Tyr His
1190 1195 1200

ATC GTG GAG CAC AGC TGG TTC GAG ACA TTC ATC ATC TTC ATG ATC 3645
Ile Val Glu His Ser Trp Phe Glu Thr Phe Ile Ile Phe Met Ile
1205 1210 1215

CTA CTC AGC AGT GGA GCG CTG GCC TTC GAG GAC ATC TAC CTA GAG 3690
Leu Leu Ser Ser Gly Ala Leu Ala Phe Glu Asp Ile Tyr Leu Glu
1220 1225 1230

GAG CGG AAG ACC ATC AAG GTT CTG CTT GAG TAT GCC GAC AAG ATG 3735
Glu Arg Lys Thr Ile Lys Val Leu Leu Glu Tyr Ala Asp Lys Met
1235 1240 1245

TTC ACA TAT GTC TTC GTG CTG GAG ATG CTG CTC AAG TGG GTG GCC 3780
Phe Thr Tyr Val Phe Val Leu Glu Met Leu Leu Lys Trp Val Ala
1250 1255 1260

TAC GGC TTC AAG AAG TAC TTC ACC AAT GCC TGG TGC TGG CTC GAC 3825
Tyr Gly Phe Lys Lys Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp
1265 1270 1275

TTC CTC ATC GTA GAC GTC TCT CTG GTC AGC CTG GTG GCC AAC ACC 3870

Phe Leu Ile Val Asp Val Ser Leu Val Ser Leu Val Ala Asn Thr
1280 1285 1290

CTG GGC TTT GCC GAG ATG GGC CCC ATC AAG TCA CTG CGG ACG CTG 3915
Leu Gly Phe Ala Glu Met Gly Pro Ile Lys Ser Leu Arg Thr Leu
1295 1300 1305

CGT GCA CTC CGT CCT CTG AGA GCT CTG TCA CGA TTT GAG GGC ATG 3960
Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser Arg Phe Glu Gly Met
1310 1315 1320

AGG GTG GTG GTC AAT GCC CTG GTG GGC GCC ATC CCG TCC ATC ATG 4005
Arg Val Val Val Asn Ala Leu Val Gly Ala Ile Pro Ser Ile Met
1325 1330 1335

AAC GTC CTC CTC GTC TGC CTC ATC TTC TGG CTC ATC TTC AGC ATC 4050
Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Ile Phe Ser Ile
1340 1345 1350

ATG GGC GTG AAC CTC TTT GCG GGG AAG TTT GGG AGG TGC ATC AAC 4095
Met Gly Val Asn Leu Phe Ala Gly Lys Phe Gly Arg Cys Ile Asn
1355 1360 1365

CAG ACA GAG GGA GAC TTG CCT TTG AAC TAC ACC ATC GTG AAC AAC 4140
Gln Thr Glu Gly Asp Leu Pro Leu Asn Tyr Thr Ile Val Asn Asn
1370 1375 1380

AAG AGC CAG TGT GAG TCC TTG AAC TTG ACC GGA GAA TTG TAC TGG 4185
Lys Ser Gln Cys Glu Ser Leu Asn Leu Thr Gly Glu Leu Tyr Trp
1385 1390 1395

ACC AAG GTG AAA GTC AAC TTT GAC AAC GTG GGG GCC GGG TAC CTG 4230
Thr Lys Val Lys Asn Phe Asp Asn Val Gly Ala Gly Tyr Leu
1400 1405 1410

GCC CTT CTG CAG GTG GCA ACA TTT AAA GGC TGG ATG GAC ATT ATG 4275
Ala Leu Leu Gln Val Ala Thr Phe Lys Gly Trp Met Asp Ile Met
1415 1420 1425

TAT GCA GCT GTG GAC TCC AGG GGG TAT GAA GAG CAG CCT CAG TGG 4320
Tyr Ala Ala Val Asp Ser Arg Gly Tyr Glu Glu Gln Pro Gln Trp
1430 1435 1440

GAA TAC AAC CTC TAC ATG TAC ATC TAT TTT GTC ATT TTC ATC ATC 4365
Glu Tyr Asn Leu Tyr Met Tyr Ile Tyr Phe Val Ile Phe Ile Ile
1445 1450 1455

TTT GGG TCT TTC ACC CTG AAC CTC TTT ATT GGT GTC ATC ATT 4410
Phe Gly Ser Phe Phe Thr Leu Asn Leu Phe Ile Gly Val Ile Ile
1460 1465 1470

GAC AAC TTC AAC CAA CAG AAG AAA AAG TTA GGG GGC CAG GAC ATC 4455
Asp Asn Phe Asn Gln Gln Lys Lys Lys Leu Gly Gly Gln Asp Ile
1475 1480 1485

TTC ATG ACA GAG GAG CAG AAG AAG TAC TAC AAT GCC ATG AAG AAG 4500

Phe Met Thr Glu Glu Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys
1490 1495 1500

CTG GGC TCC AAG AAG CCC CAG AAG CCC ATC CCA CGG CCC CTG AAC 4545
Leu Gly Ser Lys Lys Pro Gln Lys Pro Ile Pro Arg Pro Leu Asn
1505 1510 1515

AAG TAC CAG GGC TTC ATA TTC GAC ATT GTG ACC AAG CAG GCC TTT 4590
Lys Tyr Gln Gly Phe Ile Phe Asp Ile Val Thr Lys Gln Ala Phe
1520 1525 1530

GAC GTC ACC ATC ATG TTT CTG ATC TGC TTG AAT ATG GTG ACC ATG 4635
Asp Val Thr Ile Met Phe Leu Ile Cys Leu Asn Met Val Thr Met
1535 1540 1545

ATG GTG GAG ACA GAT GAC CAA AGT CCT GAG AAA ATC AAC ATC TTG 4680
Met Val Glu Thr Asp Asp Gln Ser Pro Glu Lys Ile Asn Ile Leu
1550 1555 1560

GCC AAG ATC AAC CTG CTC TTT GTG GCC ATC TTC ACA GGC GAG TGT 4725
Ala Lys Ile Asn Leu Leu Phe Val Ala Ile Phe Thr Gly Glu Cys
1565 1570 1575

ATT GTC AAG CTG GCT GCC CTG CGC CAC TAC TAC TTC ACC AAC AGC 4770
Ile Val Lys Leu Ala Ala Leu Arg His Tyr Tyr Phe Thr Asn Ser
1580 1585 1590

TGG AAT ATC TTC GAC TTC GTG GTT GTC ATC CTC TCC ATC GTG GGC 4815
Trp Asn Ile Phe Asp Phe Val Val Val Ile Leu Ser Ile Val Gly
1595 1600 1605

ACT GTG CTC TCG GAC ATC ATC CAG AAG TAC TTC TTC TCC CCG ACG 4860
Thr Val Leu Ser Asp Ile Ile Gln Lys Tyr Phe Phe Ser Pro Thr
1610 1615 1620

CTC TTC CGA GTC ATC CGC CTG GCC CGA ATA GGC CGC ATC CTC AGA 4905
Leu Phe Arg Val Ile Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg
1625 1630 1635

CTG ATC CGA GGG GCC AAG GGG ATC CGC ACG CTG CTC TTT GCC CTC 4950
Leu Ile Arg Gly Ala Lys Gly Ile Arg Thr Leu Leu Phe Ala Leu
1640 1645 1650

ATG ATG TCC CTG CCT GCC CTC TTC AAC ATC GGG CTG CTG CTC TTC 4995
Met Met Ser Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu Phe
1655 1660 1665

CTC GTC ATG TTC ATC TAC TCC ATC TTT GGC ATG GCC AAC TTC GCT 5040
Leu Val Met Phe Ile Tyr Ser Ile Phe Gly Met Ala Asn Phe Ala
1670 1675 1680

TAT GTC AAG TGG GAG GCT GGC ATC GAC GAC ATG TTC AAC TTC CAG 5085
Tyr Val Lys Trp Glu Ala Gly Ile Asp Asp Met Phe Asn Phe Gln
1685 1690 1695

ACC TTC GCC AAC AGC ATG CTG TGC CTC TTC CAG ATC ACC ACG TCG 5130

Thr Phe Ala Asn Ser Met Leu Cys Leu Phe Gln Ile Thr Thr Ser
1700 1705 1710

GCC GGC TGG GAT GGC CTC CTC AGC CCC ATC CTC AAC ACT GGG CCG 5175
Ala Gly Trp Asp Gly Leu Leu Ser Pro Ile Leu Asn Thr Gly Pro
1715 1720 1725

CCC TAC TGC GAC CCC ACT CTG CCC AAC AGC AAT GGC TCT CGG GGG 5220
Pro Tyr Cys Asp Pro Thr Leu Pro Asn Ser Asn Gly Ser Arg Gly
1730 1735 1740

GAC TGC GGG AGC CCA GCC GTG GGC ATC CTC TTC ACC ACC TAC 5265
Asp Cys Gly Ser Pro Ala Val Gly Ile Leu Phe Phe Thr Thr Tyr
1745 1750 1755

ATC ATC ATC TCC TTC CTC ATC GTG GTC AAC ATG TAC ATT GCC ATC 5310
Ile Ile Ile Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala Ile
1760 1765 1770

ATC CTG GAG AAC TTC AGC GTG GCC ACG GAG GAG AGC ACC GAG CCC 5355
Ile Leu Glu Asn Phe Ser Val Ala Thr Glu Glu Ser Thr Glu Pro
1775 1780 1785

CTG AGT GAG GAC GAC TTC GAT ATG TTC TAT GAG ATC TGG GAG AAA 5400
Leu Ser Glu Asp Asp Phe Asp Met Phe Tyr Glu Ile Trp Glu Lys
1790 1795 1800

TTT GAC CCA GAG GCC ACT CAG TTT ATT GAG TAT TCG GTC CTG TCT 5445
Phe Asp Pro Glu Ala Thr Gln Phe Ile Glu Tyr Ser Val Leu Ser
1805 1810 1815

GAC TTT GCC GAC GCC CTG TCT GAG CCA CTC CGT ATC GCC AAG CCC 5490
Asp Phe Ala Asp Ala Leu Ser Glu Pro Leu Ile Arg Ala Lys Pro
1820 1825 1830

AAC CAG ATA AGC CTC ATC AAC ATG GAC CTG CCC ATG GTG AGT GGG 5535
Asn Gln Ile Ser Leu Ile Asn Met Asp Leu Pro Met Val Ser Gly
1835 1840 1845

GAC CGC ATC CAT TGC ATG GAC ATT CTC TTT GCC TTC ACC AAA AGG 5580
Asp Arg Ile His Cys Met Asp Ile Leu Phe Ala Phe Thr Lys Arg
1850 1855 1860

GTC CTG GGG GAG TCT GGG GAG ATG GAC GCC CTG AAG ATC CAG ATG 5625
Val Leu Gly Glu Ser Gly Glu Met Asp Ala Leu Lys Ile Gln Met
1865 1870 1875

GAG GAG AAG TTC ATG GCA GCC AAC CCA TCC AAG ATC TCC TAC GAG 5670
Glu Glu Lys Phe Met Ala Ala Asn Pro Ser Lys Ile Ser Tyr Glu
1880 1885 1890

CCC ATC ACC ACC ACA CTC CGG CGC AAG CAC GAA GAG GTG TCG GCC 5715
Pro Ile Thr Thr Leu Arg Arg Lys His Glu Glu Val Ser Ala
1895 1900 1905

ATG GTT ATC CAG AGA GCC TTC CGC AGG CAC CTG CTG CAA CGC TCT 5760

Met Val Ile Gln Arg Ala Phe Arg Arg His Leu Leu Gln Arg Ser
1910 1915 1920

TTG AAG CAT GCC TCC TTC CTC CGT CAG CAG GCG GGC AGC GGC 5805
Leu Lys His Ala Ser Phe Leu Phe Arg Gln Gln Ala Gly Ser Gly
1925 1930 1935

CTC TCC GAA GAG GAT GCC CCT GAG CGA GAG GGC CTC ATC GCC TAC 5850
Leu Ser Glu Glu Asp Ala Pro Glu Arg Glu Gly Leu Ile Ala Tyr
1940 1945 1950

G TG ATG AGT GAG AAC TTC TCC CGA CCC CTT GGC CCA CCC TCC AGC 5895
Val Met Ser Glu Asn Phe Ser Arg Pro Leu Gly Pro Pro Ser Ser
1955 1960 1965

TCC TCC ATC TCC TCC ACT TCC TTC CCA CCC TCC TAT GAC AGT GTC 5940
Ser Ser Ile Ser Ser Thr Ser Phe Pro Pro Ser Tyr Asp Ser Val
1970 1975 1980

ACT AGA GCC ACC AGC GAT AAC CTC CAG GTG CGG GGG TCT GAC TAC 5985
Thr Arg Ala Thr Ser Asp Asn Leu Gln Val Arg Gly Ser Asp Tyr
1985 1990 1995

AGC CAC AGT GAA GAT CTC GCC GAC TTC CCC CCT TCT CCG GAC AGG 6030
Ser His Ser Glu Asp Leu Ala Asp Phe Pro Pro Ser Pro Asp Arg
2000 2005 2010

GAC CGT GAG TCC ATC GTG 6048
Asp Arg Glu Ser Ile Val
2015

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2016 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Asn Phe Leu Leu Pro Arg Gly Thr Ser Ser Phe Arg Arg
1 5 10 15

Phe Thr Arg Glu Ser Leu Ala Ala Ile Glu Lys Arg Met Ala Glu
20 25 30

Lys Gln Ala Arg Gly Ser Thr Thr Leu Gln Glu Ser Arg Glu Gly
35 40 45

Leu Pro Glu Glu Ala Pro Arg Pro Gln Leu Asp Leu Gln Ala
50 55 60

Ser Lys Lys Leu Pro Asp Leu Tyr Gly Asn Pro Pro Gln Glu Leu
65 70 75

Ile Gly Glu Pro Leu Glu Asp Leu Asp Pro Phe Tyr Ser Thr Gln

80	85	90
Lys Thr Phe Ile Val Leu Asn Lys Gly Lys	Thr Ile Phe Arg Phe	
95	100	105
Ser Ala Thr Asn Ala Leu Tyr Val Leu Ser Pro Phe His Pro Val		
110	115	120
Arg Arg Ala Ala Val Lys Ile Leu Val His Ser Leu Phe Asn Met		
125	130	135
Leu Ile Met Cys Thr Ile Leu Thr Asn Cys Val Phe Met Ala Gln		
140	145	150
His Asp Pro Pro Trp Thr Lys Tyr Val Glu Tyr Thr Phe Thr		
155	160	165
Ala Ile Tyr Thr Phe Glu Ser Leu Val Lys Ile Leu Ala Arg Ala		
170	175	180
Phe Cys Leu His Ala Phe Thr Phe Leu Arg Asp Pro Trp Asn Trp		
185	190	195
Leu Asp Phe Ser Val Ile Ile Met Ala Tyr Thr Thr Glu Phe Val		
200	205	210
Asp Leu Gly Asn Val Ser Ala Leu Arg Thr Phe Arg Val Leu Arg		
215	220	225
Ala Leu Lys Thr Ile Ser Val Ile Ser Gly Leu Lys Thr Ile Val		
230	235	240
Gly Ala Leu Ile Gln Ser Val Lys Lys Leu Ala Asp Val Met Val		
245	250	255
Leu Thr Val Phe Cys Leu Ser Val Phe Ala Leu Ile Gly Leu Gln		
260	265	270
Leu Phe Met Gly Asn Leu Arg His Lys Cys Val Arg Asn Phe Thr		
275	280	285
Ala Leu Asn Gly Thr Asn Gly Ser Val Glu Ala Asp Gly Leu Val		
290	295	300
Trp Glu Ser Leu Asp Leu Tyr Leu Ser Asp Pro Glu Asn Tyr Leu		
305	310	315
Leu Lys Asn Gly Thr Ser Asp Val Leu Leu Cys Gly Asn Ser Ser		
320	325	330
Asp Ala Gly Thr Cys Pro Glu Gly Tyr Arg Cys Leu Lys Ala Gly		
335	340	345
Glu Asn Pro Asp His Gly Tyr Thr Ser Phe Asp Ser Phe Ala Trp		
350	355	360

Ala Phe Leu Ala Leu Phe Arg Leu Met Thr Gln Asp Cys Trp Glu
365 370 375

Arg Leu Tyr Gln Gln Thr Leu Arg Ser Ala Gly Lys Ile Tyr Met
380 385 390

Ile Phe Phe Met Leu Val Ile Phe Leu Gly Ser Phe Tyr Leu Val
395 400 405

Asn Leu Ile Leu Ala Val Val Ala Met Ala Tyr Glu Glu Gln Asn
410 415 420

Gln Ala Thr Ile Ala Glu Thr Glu Glu Lys Glu Lys Arg Phe Gln
425 430 435

Glu Ala Met Glu Met Leu Lys Lys Glu His Glu Ala Leu Thr Ile
440 445 450

Arg Gly Val Asp Thr Val Ser Arg Ser Ser Leu Glu Met Ser Pro
455 460 465

Leu Ala Pro Val Asn Ser His Glu Arg Arg Ser Lys Arg Arg Lys
470 475 480

Arg Met Ser Ser Gly Thr Glu Glu Cys Gly Glu Asp Arg Leu Pro
485 490 495

Lys Ser Asp Ser Glu Asp Gly Pro Arg Ala Met Asn His Leu Ser
500 505 510

Leu Thr Arg Gly Leu Ser Arg Thr Ser Met Lys Pro Arg Ser Ser
515 520 525

Arg Gly Ser Ile Phe Thr Phe Arg Arg Asp Leu Gly Ser Glu
530 535 540

Ala Asp Phe Ala Asp Asp Glu Asn Ser Thr Ala Arg Glu Ser Glu
545 550 555

Ser His His Thr Ser Leu Leu Val Pro Trp Pro Leu Arg Arg Thr
560 565 570

Ser Ala Gln Gly Gln Pro Ser Pro Gly Thr Ser Ala Pro Gly His
575 580 585

Ala Leu His Gly Lys Lys Asn Ser Thr Val Asp Cys Asn Gly Val
590 595 600

Val Ser Leu Leu Gly Ala Gly Asp Pro Glu Ala Thr Ser Pro Gly
605 610 615

Ser His Leu Leu Arg Pro Val Met Leu Glu His Pro Pro Asp Thr
620 625 630

Thr Thr Pro Ser Glu Glu Pro Gly Gly Pro Gln Met Leu Thr Ser
635 640 645

Gln Ala Pro Cys Val Asp Gly Phe Glu Glu Pro Gly Ala Arg Gln
650 655 660

Arg Ala Leu Ser Ala Val Ser Val Leu Thr Ser Ala Leu Glu Glu
665 670 675

Leu Glu Glu Ser Arg His Lys Cys Pro Pro Cys Trp Asn Arg Leu
680 685 690

Ala Gln Arg Tyr Leu Ile Trp Glu Cys Cys Pro Leu Trp Met Ser
695 700 705

Ile Lys Gln Gly Val Lys Leu Val Val Met Asp Pro Phe Thr Asp
710 715 720

Leu Thr Ile Thr Met Cys Ile Val Leu Asn Thr Leu Phe Met Ala
725 730 735

Leu Glu His Tyr Asn Met Thr Ser Glu Phe Glu Glu Met Leu Gln
740 745 750

Val Gly Asn Leu Val Phe Thr Gly Ile Phe Thr Ala Glu Met Thr
755 760 765

Phe Lys Ile Ile Ala Leu Asp Pro Tyr Tyr Phe Gln Gln Gly
770 775 780

Trp Asn Ile Phe Asp Ser Ile Ile Val Ile Leu Ser Leu Met Glu
785 790 795

Leu Gly Leu Ser Arg Met Ser Asn Leu Ser Val Leu Arg Ser Phe
800 805 810

Arg Leu Leu Arg Val Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu
815 820 825

Asn Thr Leu Ile Lys Ile Ile Gly Asn Ser Val Gly Ala Leu Gly
830 835 840

Asn Leu Thr Leu Val Leu Ala Ile Ile Val Phe Ile Phe Ala Val
845 850 855

Val Gly Met Gln Leu Phe Gly Lys Asn Tyr Ser Glu Leu Arg Asp
860 865 870

Ser Asp Ser Gly Leu Leu Pro Arg Trp His Met Met Asp Phe Phe
875 880 885

His Ala Phe Leu Ile Ile Phe Arg Ile Leu Cys Gly Glu Trp Ile
890 895 900

Glu Thr Met Trp Asp Cys Met Glu Val Ser Gly Gln Ser Leu Cys
905 910 915

Leu Leu Val Phe Leu Leu Val Met Val Ile Gly Asn Leu Val Val
920 925 930

Leu Asn Leu Phe Leu Ala Leu Leu Ser Ser Phe Ser Ala Asp
935 940 945

Asn Leu Thr Ala Pro Asp Glu Asp Arg Glu Met Asn Asn Leu Gln
950 955 960

Leu Ala Leu Ala Arg Ile Gln Arg Gly Leu Arg Phe Val Lys Arg
965 970 975

Thr Thr Trp Asp Phe Cys Cys Gly Leu Leu Arg His Arg Pro Gln
980 985 990

Lys Pro Ala Ala Leu Ala Ala Gln Gly Gln Leu Pro Ser Cys Ile
995 1000 1005

Ala Thr Pro Tyr Ser Pro Pro Pro Glu Thr Glu Lys Val Pro
1010 1015 1020

Pro Thr Arg Lys Glu Thr Gln Phe Glu Glu Gly Glu Gln Pro Gly
1025 1030 1035

Gln Gly Thr Pro Gly Asp Pro Glu Pro Val Cys Val Pro Ile Ala
1040 1045 1050

Val Ala Glu Ser Asp Thr Asp Asp Gln Glu Glu Asp Glu Glu Asn
1055 1060 1065

Ser Leu Gly Thr Glu Glu Glu Ser Ser Lys Gln Gln Glu Ser Gln
1070 1075 1080

Pro Val Ser Gly Trp Pro Arg Gly Pro Pro Asp Ser Arg Thr Trp
1085 1090 1095

Ser Gln Val Ser Ala Thr Ala Ser Ser Glu Ala Glu Ala Ser Ala
1100 1105 1110

Ser Gln Ala Asp Trp Arg Gln Gln Trp Lys Ala Glu Pro Gln Ala
1115 1120 1125

Pro Gly Cys Gly Glu Thr Pro Glu Asp Ser Cys Ser Glu Gly Ser
1130 1135 1140

Thr Ala Asp Met Thr Asn Thr Ala Glu Leu Leu Glu Gln Ile Pro
1145 1150 1155

Asp Leu Gly Gln Asp Val Lys Asp Pro Glu Asp Cys Phe Thr Glu
1160 1165 1170

Gly Cys Val Arg Arg Cys Pro Cys Cys Ala Val Asp Thr Thr Gln
1175 1180 1185

Ala Pro Gly Lys Val Trp Trp Arg Leu Arg Lys Thr Cys Tyr His
1190 1195 1200

Ile Val Glu His Ser Trp Phe Glu Thr Phe Ile Ile Phe Met Ile
1205 1210 1215

Leu Leu Ser Ser Gly Ala Leu Ala Phe Glu Asp Ile Tyr Leu Glu
1220 1225 1230

Glu Arg Lys Thr Ile Lys Val Leu Leu Glu Tyr Ala Asp Lys Met
1235 1240 1245

Phe Thr Tyr Val Phe Val Leu Glu Met Leu Leu Lys Trp Val Ala
1250 1255 1260

Tyr Gly Phe Lys Lys Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp
1265 1270 1275

Phe Leu Ile Val Asp Val Ser Leu Val Ser Leu Val Ala Asn Thr
1280 1285 1290

Leu Gly Phe Ala Glu Met Gly Pro Ile Lys Ser Leu Arg Thr Leu
1295 1300 1305

Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser Arg Phe Glu Gly Met
1310 1315 1320

Arg Val Val Val Asn Ala Leu Val Gly Ala Ile Pro Ser Ile Met
1325 1330 1335

Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Ile Phe Ser Ile
1340 1345 1350

Met Gly Val Asn Leu Phe Ala Gly Lys Phe Gly Arg Cys Ile Asn
1355 1360 1365

Gln Thr Glu Gly Asp Leu Pro Leu Asn Tyr Thr Ile Val Asn Asn
1370 1375 1380

Lys Ser Gln Cys Glu Ser Leu Asn Leu Thr Gly Glu Leu Tyr Trp
1385 1390 1395

Thr Lys Val Lys Val Asn Phe Asp Asn Val Gly Ala Gly Tyr Leu
1400 1405 1410

Ala Leu Leu Gln Val Ala Thr Phe Lys Gly Trp Met Asp Ile Met
1415 1420 1425

Tyr Ala Ala Val Asp Ser Arg Gly Tyr Glu Glu Gln Pro Gln Trp
1430 1435 1440

Glu Tyr Asn Leu Tyr Met Tyr Ile Tyr Phe Val Ile Phe Ile Ile
1445 1450 1455

Phe Gly Ser Phe Phe Thr Leu Asn Leu Phe Ile Gly Val Ile Ile
1460 1465 1470

Asp Asn Phe Asn Gln Gln Lys Lys Lys Leu Gly Gly Gln Asp Ile
1475 1480 1485

Phe Met Thr Glu Glu Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys
1490 1495 1500

Leu Gly Ser Lys Lys Pro Gln Lys Pro Ile Pro Arg Pro Leu Asn
1505 1510 1515

Lys Tyr Gln Gly Phe Ile Phe Asp Ile Val Thr Lys Gln Ala Phe
1520 1525 1530

Asp Val Thr Ile Met Phe Leu Ile Cys Leu Asn Met Val Thr Met
1535 1540 1545

Met Val Glu Thr Asp Asp Gln Ser Pro Glu Lys Ile Asn Ile Leu
1550 1555 1560

Ala Lys Ile Asn Leu Leu Phe Val Ala Ile Phe Thr Gly Glu Cys
1565 1570 1575

Ile Val Lys Leu Ala Ala Leu Arg His Tyr Tyr Phe Thr Asn Ser
1580 1585 1590

Trp Asn Ile Phe Asp Phe Val Val Val Ile Leu Ser Ile Val Gly
1595 1600 1605

Thr Val Leu Ser Asp Ile Ile Gln Lys Tyr Phe Phe Ser Pro Thr
1610 1615 1620

Leu Phe Arg Val Ile Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg
1625 1630 1635

Leu Ile Arg Gly Ala Lys Gly Ile Arg Thr Leu Leu Phe Ala Leu
1640 1645 1650

Met Met Ser Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu Leu Phe
1655 1660 1665

Leu Val Met Phe Ile Tyr Ser Ile Phe Gly Met Ala Asn Phe Ala
1670 1675 1680

Tyr Val Lys Trp Glu Ala Gly Ile Asp Asp Met Phe Asn Phe Gln
1685 1690 1695

Thr Phe Ala Asn Ser Met Leu Cys Leu Phe Gln Ile Thr Thr Ser
1700 1705 1710

Ala Gly Trp Asp Gly Leu Leu Ser Pro Ile Leu Asn Thr Gly Pro
1715 1720 1725

Pro Tyr Cys Asp Pro Thr Leu Pro Asn Ser Asn Gly Ser Arg Gly
1730 1735 1740

Asp Cys Gly Ser Pro Ala Val Gly Ile Leu Phe Phe Thr Thr Tyr
1745 1750 1755

Ile Ile Ile Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala Ile
1760 1765 1770

Ile Leu Glu Asn Phe Ser Val Ala Thr Glu Glu Ser Thr Glu Pro
1775 1780 1785

Leu Ser Glu Asp Asp Phe Asp Met Phe Tyr Glu Ile Trp Glu Lys
1790 1795 1800

Phe Asp Pro Glu Ala Thr Gln Phe Ile Glu Tyr Ser Val Leu Ser
1805 1810 1815

Asp Phe Ala Asp Ala Leu Ser Glu Pro Leu Ile Arg Ala Lys Pro
1820 1825 1830

Asn Gln Ile Ser Leu Ile Asn Met Asp Leu Pro Met Val Ser Gly
1835 1840 1845

Asp Arg Ile His Cys Met Asp Ile Leu Phe Ala Phe Thr Lys Arg
1850 1855 1860

Val Leu Gly Glu Ser Gly Glu Met Asp Ala Leu Lys Ile Gln Met
1865 1870 1875

Glu Glu Lys Phe Met Ala Ala Asn Pro Ser Lys Ile Ser Tyr Glu
1880 1885 1890

Pro Ile Thr Thr Leu Arg Arg Lys His Glu Glu Val Ser Ala
1895 1900 1905

Met Val Ile Gln Arg Ala Phe Arg Arg His Leu Leu Gln Arg Ser
1910 1915 1920

Leu Lys His Ala Ser Phe Leu Phe Arg Gln Gln Ala Gly Ser Gly
1925 1930 1935

Leu Ser Glu Glu Asp Ala Pro Glu Arg Glu Gly Leu Ile Ala Tyr
1940 1945 1950

Val Met Ser Glu Asn Phe Ser Arg Pro Leu Gly Pro Pro Ser Ser
1955 1960 1965

Ser Ser Ile Ser Ser Thr Ser Phe Pro Pro Ser Tyr Asp Ser Val
1970 1975 1980

Thr Arg Ala Thr Ser Asp Asn Leu Gln Val Arg Gly Ser Asp Tyr
1985 1990 1995

Ser His Ser Glu Asp Leu Ala Asp Phe Pro Pro Ser Pro Asp Arg
2000 2005 2010

Asp Arg Glu Ser Ile Val
2015

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGCAAACCT TCCTATTACC TCGG 24

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CACGATGGAC TCACGGTCCC TGTC 24

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3069 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GGG AAG GGG GTT GGA CGT GAT AAG TAT GAG CCT GCA GCT GTT 45
Met Gly Lys Gly Val Gly Arg Asp Lys Tyr Glu Pro Ala Ala Val
1 5 10 15

TCA GAA CAA GGT GAT AAA AAG GGC AAA AAG GGC AAA AAA GAC AGG 90
Ser Glu Gln Glu Asp Lys Lys Glu Lys Lys Glu Lys Lys Asp Arg
20 25 30

GAC ATG GAT GAA CTG AAG AAA GAA GTT TCT ATG GAT GAT CAT AAA 135
Asp Met Asp Glu Leu Lys Lys Glu Val Ser Met Asp Asp His Lys
35 40 45

CTT AGC CTT GAT GAA CTT CAT CGT AAA TAT GGA ACA GAC TTG AGC 180
Leu Ser Leu Asp Glu Leu His Arg Lys Tyr Gly Thr Asp Leu Ser
50 55 60

CGG GGA TTA ACA TCT GCT CGT GCA GCT GAG ATC CTG GCG CGA GAT Arg Gly Leu Thr Ser Ala Arg Ala Ala Glu Ile Leu Ala Arg Asp	65	70	75	225
GGT CCC AAC GCC CTC ACT CCC CCT CCC ACT ACT CCT GAA TGG ATC Gly Pro Asn Ala Leu Thr Pro Pro Pro Thr Thr Pro Glu Trp Ile	80	85	90	270
AAG TTT TGT CGG CAG CTC TTT GGG GGG TTC TCA ATG TTA CTG TGG Lys Phe Cys Arg Gln Leu Phe Gly Gly Phe Ser Met Leu Leu Trp	95	100	105	315
ATT GGA GCG ATT CTT TGT TTC TTG GCT TAT AGC ATC CAA GCT GCT Ile Gly Ala Ile Leu Cys Phe Leu Ala Tyr Ser Ile Gln Ala Ala	110	115	120	360
ACA GAA GAG GAA CCT CAA AAC GAT AAT CTG TAC CTG GGT GTG GTG Thr Glu Glu Glu Pro Gln Asn Asp Asn Leu Tyr Leu Gly Val Val	125	130	135	405
CTA TCA GCC GTT GTA ATC ATA ACT GGT TGC TTC TCC TAC TAT CAA Leu Ser Ala Val Val Ile Ile Thr Gly Cys Phe Ser Tyr Tyr Gln	140	145	150	450
GAA GCT AAA AGT TCA AAG ATC ATG GAA TCC TTC AAA AAC ATG GTC Glu Ala Lys Ser Ser Lys Ile Met Glu Ser Phe Lys Asn Met Val	155	160	165	495
CCT CAG CAA GCC CTT GTG ATT CGA AAT GGT GAG AAA ATG AGC ATA Pro Gln Gln Ala Leu Val Ile Arg Asn Gly Glu Lys Met Ser Ile	170	175	180	540
AAT GCG GAG GAA GTT GTG GTT GGG GAT CTG GTG GAA GTA AAA GGA Asn Ala Glu Glu Val Val Val Gly Asp Lue Val Glu Val Lys Gly	185	190	195	585
GGA GAC CGA ATT CCT GCT GAC CTC AGA ATC ATA TCT GCA AAT GGC Gly Asp Arg Ile Pro Ala Asp Leu Arg Ile Ile Ser Ala Asn Gly	200	205	210	630
TGC AAG GTG GAT AAC TCC TCG CTC ACT GGT GAA TCA GAA CCC CAG Cys Lys Val Asp Asn Ser Ser Leu Thr Gly Glu Ser Glu Pro Gln	215	220	225	675
ACT AGG TCT CCA GAT TTC ACA AAT GAA AAC CCC CTG GAG ACG AGG Thr Arg Ser Pro Asp Phe Thr Asn Glu Asn Pro Leu Glu Thr Arg	230	235	240	720
AAC ATT GCC TTC TTT TCA ACA AAT TGT GTT GAA GGC ACC GCA CGT Asn Ile Ala Phe Phe Ser Thr Asn Cys Val Glu Gly Thr Ala Arg	245	250	255	765
GGT ATT GTT GTC TAC ACT GGG GAT CGC ACT GTG ATG GGA AGA ATT Gly Ile Val Val Tyr Thr Gly Asp Arg Thr Val Met Gly Arg Ile	260	265	270	810

GCC ACA CTT GCT TCT GGG CTG GAA GGA GGC CAG ACC CCC ATT GCT		855
Ala Thr Leu Ala Ser Gly Leu Glu Gly Gly Gln Thr Pro Ile Ala		
275	280	285
GCA GAA ATT GAA CAT TTT ATC CAC ATC ATC ACG GGT GTG GCT GTG		900
Ala Glu Ile Glu His Phe Ile His Ile Ile Thr Gly Val Ala Val		
290	295	300
TTC CTG GGT GTG TCT TTC TTC ATC CTT TCT CTC ATC CTT GAG TAC		945
Phe Leu Gly Val Ser Phe Phe Ile Leu Ser Leu Ile Leu Glu Tyr		
305	310	315
ACC TGG CTT GAG GCT GTC ATC TTC CTC ATC GGT ATC ATC GTA GCC		990
Thr Trp Leu Glu Ala Val Ile Phe Leu Ile Gly Ile Ile Val Ala		
320	325	330
AAT GTG CCG GAA GGT TTG CTG GCC ACT GTC ACG GTC TGT CTG ACA		1035
Asn Val Pro Glu Gly Leu Leu Ala Thr Val Thr Val Cys Leu Thr		
335	340	345
CTT ACT GCC AAA CGC ATG GCA AGG AAA AAC TGC TTA GTG AAG AAC		1080
Leu Thr Ala Lys Arg Met Ala Arg Lys Asn Cys Leu Val Lys Asn		
350	355	360
TTA GAA GCT GTG GAG ACC TTG GGG TCC ACG TCC ACC ATC TGC TCT		1125
Leu Glu Ala Val Glu Thr Leu Gly Ser Thr Ser Thr Ile Cys Ser		
365	370	375
GAT AAA ACT GGA ACT CTG ACT CAG AAC CGG ATG ACA GTG GCC CAC		1170
Asp Lys Thr Gly Thr Leu Thr Gln Asn Arg Met Thr Val Ala His		
380	385	390
ATG TGG TTT GAC AAT CAA ATC CAT GAA GCT GAT ACG ACA GAG AAT		1215
Met Trp Phe Asp Asn Gln Ile His Glu Ala Asp Thr Thr Glu Asn		
395	400	405
CAG AGT GGT GTC TCT TTT GAC AAG ACT TCA GCT ACC TGG CTT GCT		1260
Gln Ser Gly Val Ser Phe Asp Lys Thr Ser Ala Thr Trp Leu Ala		
410	415	420
CTG TCC AGA ATT GCA GGT CTT TGT AAC AGG GCA GTG TTT CAG GCT		1305
Leu Ser Arg Ile Ala Gly Leu Cys Asn Arg Ala Val Phe Gln Ala		
425	430	435
AAC CAG GAA AAC CTA CCT ATT CTT AAG CGG GCA GTT GCA GGA GAT		1350
Asn Gln Glu Asn Leu Pro Ile Leu Lys Arg Ala Val Ala Gly Asp		
440	445	450
GCC TCT GAG TCA GCA CTC TTA AAG TGC ATA GAG CTG TGC TGT GGT		1395
Ala Ser Glu Ser Ala Leu Leu Lys Cys Ile Glu Leu Cys Cys Gly		
455	460	465
TTC GTG AAG GAG ATG AGA GAA AGA TAC GCC AAA ATC GTC GAG ATA		1440
Ser Val Lys Glu Met Arg Glu Arg Tyr Ala Lys Ile Val Glu Ile		
470	475	480

CCC TTC AAC TCC ACC AAC AAG TAC CAG TTG TCT ATT CAT AAG AAC 1485
Pro Phe Asn Ser Thr Asn Lys Tyr Gln Leu Ser Ile His Lys Asn
485 490 495

CCC AAC ACA TCG GAG CCC CAA CAC CTG TTG GTG ATG AAG GGC GCC 1520
Pro Asn Thr Ser Glu Pro Gln His Leu Leu Val Met Lys Gly Ala
500 505 510

CCA GAA AGG ATC CTA GAC CGT TGC AGC TCT ATC CTC CTC CAC GGC 1565
Pro Glu Arg Ile Leu Asp Arg Cys Ser Ser Ile Leu Leu His Gly
515 520 525

AAG GAG CAG CCC CTG GAT GAG CTG AAA GAC GCC TTT CAG AAC 1620
Lys Glu Gln Pro Leu Asp Glu Glu Leu Lys Asp Ala Phe Gln Asn
530 535 540

GCC TAT TTG GAG CTG GGG GGC CTC GGA GAA CGA GTC CTA GGT TTC 1665
Ala Tyr Leu Glu Leu Gly Leu Gly Glu Arg Val Leu Gly Phe
545 550 555

TGC CAC CTC TTT CTG CCA GAT GAA CAG TTT CCT GAA GGG TTC CAG 1710
Cys His Leu Phe Leu Pro Asp Glu Gln Phe Pro Glu Gly Phe Gln
560 565 570

TTT GAC ACT GAC GAT GTG AAT TTC CCT ATC GAT AAT CTG TGC TTC 1755
Phe Asp Thr Asp Asp Val Asn Phe Pro Ile Asp Asn Leu Cys Phe
575 580 585

GTT GGG CTC ATC TCC ATG ATT GAC CCT CCA CGG GCG GCC GTT CCT 1800
Val Gly Leu Ile Ser Met Ile Asp Pro Pro Arg Ala Ala Val Pro
590 595 600

GAT GCC GTG GGC AAA TGT CGA AGT GCT GGA ATT AAG GTC ATC ATG 1845
Asp Ala Val Gly Lys Cys Arg Ser Aal Gly Ile Lys Val Ile Met
605 610 615

GTC ACA GGA GAC CAT CCA ATC ACA GCT AAA GCT ATT GCC AAA GGT 1890
Val Thr Gly Asp His Pro Ile Thr Ala Lys Ala Ile Ala Lys Gly
620 625 630

GTC GGC ATC ATC TCA GAA GGC ATG GAG ACC GTG GAA GAC ATT GCT 1935
Val Gly Ile Ile Ser Glu Gly Asn Glu Thr Val Glu Asp Ile Ala
635 640 645

GCC CGC CTC AAC ATC CCA GTC AGC CAG GTG AAC CCC AGG GAT GCC 1980
Ala Arg Leu Asn Ile Pro Val Ser Gln Val Asn Pro Arg Asp Ala
650 655 660

AAG GCC TGC GTA GTA CAC GGC AGT GAT CTA AAG GAC ATG ACC TCC 2025
Lys Ala Cys Val Val His Gly Ser Asp Leu Lys Asp Met Thr Ser
665 670 675

GAG CAG CTG GAT GAC ATT TTG AAG TAC CAC ACT GAG ATA GTG TTT 2070
Glu Glu Leu Asp Asp Ile Leu Lys Tyr His Thr Glu Ile Val Phe
680 685 690

GCC AGG ACC TCC CCT CAG CAG AAG CTC ATC ATT GTG GAA GGC TGC Ala Arg Thr Ser Pro Gln Gln Lys Leu Ile Ile Val Glu Gly Cys 695 700 705	2115
CAA AGA CAG GGT GCT ATC GTG GCT GTG ACT GGT GAC GGT GTG AAT Gln Arg Gln Gly Ala Ile Val Ala Val Thr Gly Asp Gly Val Asn 710 715 720	2160
GAC TCT CCA GCT TTG AAG AAA GCA GAC ATT GGG GTT GCT ATG GGG Asp Ser Pro Ala Leu Lys Lys Ala Asp Ile Gly Val Ala Met Gly 725 730 735	2205
ATT GCT GGC TCA GAT GTG TCC AAG CAA GCT GCT GAC ATG ATT CTT Ile Ala Gly Ser Asp Val Ser Lys Gln Ala Ala Asp Met Ile Leu 740 745 750	2250
CTG GAT GAC AAC TTT GCC TCA ATT GTG ACT GGA GTA GAG GAA GGT Leu Asp Asp Asn Phe Ala Ser Ile Val Thr Gly Val Glu Glu Gly 755 760 765	2295
CGT CTG ATC TTT GAT AAC TTG AAG AAA TCC ATT GCT TAT ACC TTA Arg Leu Ile Phe Asp Asn Leu Lys Lys Ser Ile Ala Tyr Thr Leu 770 775 780	2340
ACC AGT AAC ATT CCC GAG ATC ACC CCG TTC CTG ATA TTT ATT ATT Thr Ser Asn Ile Pro Glu Ile Thr Pro Phe Leu Ile Phe Ile Ile 785 790 795	2385
GCA AAC ATT CCA CTA CCA CTG GGG ACT GTC ACC ATC CTC TGC ATT Ala Asn Ile Pro Leu Pro Leu Gly Thr Val Thr Ile Leu Cys Ile 800 805 810	2430
GAC TTG GGC ACT GAC ATG GTT CCT GCC ATC TCC CTG GCT TAT GAG Asp Leu Gly Thr Asp Met Val Pro Ala Ile Ser Leu Ala Tyr Glu 815 820 825	2475
CAG GCT GAG AGT GAC ATC ATG AAG AGA CAG CCC AGA AAT CCC AAA Gln Ala Glu Ser Asp Ile Met Lys Arg Gln Pro Arg Asn Pro Lys 830 835 840	2520
ACA GAC AAA CTT GTG AAT GAG CGG CTG ATC AGC ATG GCC TAT GGG Thr Asp Lys Leu Val Asn Glu Arg Leu Ile Ser Met Ala Tyr Gly 845 850 855	2565
CAG ATT GGA ATG ATC CAG GCC CTG GGA GGC TTC TTT ACT TAC TTT Gln Ile Gly Met Ile Gln Ala Leu Gly Gly Phe Phe Thr Tyr Phe 860 865 870	2610
GTG ATT CTG GCT GAG AAC GGC TTC CTC CCA ATT CAC CTG TTG GGC Val Ile Leu Ala Glu Asn Gly Phe Leu Pro Ile His Leu Leu Gly 875 880 885	2655
CTC CGA GTG GAC TGG GAT GAC CGC TGG ATC AAC GAT GTG GAA GAC Leu Arg Val Asp Trp Asp Asp Arg Trp Ile Asn Asp Val Glu Asp	2700

890	895	900	
AGC TAC GGG CAG CAG TGG ACC TAT GAG CAG AGG AAA ATC GTG GAG	2745		
Ser Tyr Gly Gln Gln Trp Thr Tyr Glu Gln Arg Lys Ile Val Glu			
905	910	915	
TTC ACC TGC CAC ACA GCC TTC TTC GTC AGT ATC GTG GTG GTG CAG	2790		
Phe Thr Cys His Thr Ala Phe Phe Val Ser Ile Val Val Val Gln			
920	925	930	
TGG GCC GAC TTG GTC ATC TGT AAG ACC AGG AGG AAT TCG GTC TTC	2835		
Trp Ala Asp Leu Val Ile Cys Lys Thr Arg Arg Asn Ser Val Phe			
935	940	945	
CAG CAG GGG ATG AAG AAC AAG ATC TTG ATA TTT GGC CTC TTT GAA	2880		
Gln Gln Gly Met Lys Asn Lys Ile Leu Ile Phe Gly Leu Phe Glu			
950	955	960	
GAG ACA GCC CTG GCT GCT TTC CTT TCC TAC TGC CCT GGA ATG GGT	2925		
Glu Thr Ala Leu Ala Ala Phe Leu Ser Tyr Cys Pro Gly Met Gly			
965	970	975	
GTT GCT CTT AGG ATG TAT CCC CTC AAA CCT ACC TGG TGG TTC TGT	2970		
Val Ala Leu Arg Met Tyr Pro Leu Lys Pro Thr Trp Trp Phe Cys			
980	985	990	
GCC TTC CCC TAC TCT CTT CTC ATC TTC GTA TAT GAC GAA GTC AGA	3015		
Ala Phe Pro Tyr Ser Leu Leu Ile Phe Val Tyr Asp Glu Val Arg			
995	1000	1005	
AAA CTC ATC ATC AGG CGA CGC CCT GGC GGC TGG GTG GAG AAG GAA	3060		
Lys Leu Ile Ile Arg Arg Arg Pro Gly Gly Trp Val Glu Lys Glu			
1010	1015	1020	
ACC TAC TAT 3069			
Thr Tyr Tyr			

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1023 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Lys Gly Val Gly Arg Asp Lys Tyr Glu Pro Ala Ala Val
1 5 10 15

Ser Glu Gln Glu Asp Lys Lys Glu Lys Lys Glu Lys Lys Asp Arg
20 25 30

Asp Met Asp Glu Leu Lys Lys Glu Val Ser Met Asp Asp His Lys
35 40 45

Leu Ser Leu Asp Glu Leu His Arg Lys Tyr Gly Thr Asp Leu Ser

50	55	60
Arg Gly Leu Thr Ser Ala Arg Ala Ala Glu Ile Leu Ala Arg Asp		
65	70	75
Gly Pro Asn Ala Leu Thr Pro Pro Pro Thr Thr Pro Glu Trp Ile		
80	85	90
Lys Phe Cys Arg Gln Leu Phe Gly Gly Phe Ser Met Leu Leu Trp		
95	100	105
Ile Gly Ala Ile Leu Cys Phe Leu Ala Tyr Ser Ile Gln Ala Ala		
110	115	120
Thr Glu Glu Glu Pro Gln Asn Asp Asn Leu Tyr Leu Gly Val Val		
125	130	135
Leu Ser Ala Val Val Ile Ile Thr Gly Cys Phe Ser Tyr Tyr Gln		
140	145	150
Glu Ala Lys Ser Ser Lys Ile Met Glu Ser Phe Lys Asn Met Val		
155	160	165
Pro Gln Gln Ala Leu Val Ile Arg Asn Gly Glu Lys Met Ser Ile		
170	175	180
Asn Ala Glu Glu Val Val Val Gly Asp Lue Val Glu Val Lys Gly		
185	190	195
Gly Asp Arg Ile Pro Ala Asp Leu Arg Ile Ile Ser Ala Asn Gly		
200	205	210
Cys Lys Val Asp Asn Ser Ser Leu Thr Gly Glu Ser Glu Pro Gln		
215	220	225
Thr Arg Ser Pro Asp Phe Thr Asn Glu Asn Pro Leu Glu Thr Arg		
230	235	240
Asn Ile Ala Phe Phe Ser Thr Asn Cys Val Glu Gly Thr Ala Arg		
245	250	255
Gly Ile Val Val Tyr Thr Gly Asp Arg Thr Val Met Gly Arg Ile		
260	265	270
Ala Thr Leu Ala Ser Gly Leu Glu Gly Gly Gln Thr Pro Ile Ala		
275	280	285
Ala Glu Ile Glu His Phe Ile His Ile Ile Thr Gly Val Ala Val		
290	295	300
Phe Leu Gly Val Ser Phe Phe Ile Leu Ser Leu Ile Leu Glu Tyr		
305	310	315
Thr Trp Leu Glu Ala Val Ile Phe Leu Ile Gly Ile Ile Val Ala		

320	325	330
Asn Val Pro Glu Gly Leu Leu Ala Thr Val Thr Val Cys Leu Thr		
335	340	345
Leu Thr Ala Lys Arg Met Ala Arg Lys Asn Cys Leu Val Lys Asn		
350	355	360
Leu Glu Ala Val Glu Thr Leu Gly Ser Thr Ser Thr Ile Cys Ser		
365	370	375
Asp Lys Thr Gly Thr Leu Thr Gln Asn Arg Met Thr Val Ala His		
380	385	390
Met Trp Phe Asp Asn Gln Ile His Glu Ala Asp Thr Thr Glu Asn		
395	400	405
Gln Ser Gly Val Ser Phe Asp Lys Thr Ser Ala Thr Trp Leu Ala		
410	415	420
Leu Ser Arg Ile Ala Gly Leu Cys Asn Arg Ala Val Phe Gln Ala		
425	430	435
Asn Gln Glu Asn Leu Pro Ile Leu Lys Arg Ala Val Ala Gly Asp		
440	445	450
Ala Ser Glu Ser Ala Leu Leu Lys Cys Ile Glu Leu Cys Cys Gly		
455	460	465
Ser Val Lys Glu Met Arg Glu Arg Tyr Ala Lys Ile Val Glu Ile		
470	475	480
Pro Phe Asn Ser Thr Asn Lys Tyr Gln Leu Ser Ile His Lys Asn		
485	490	495
Pro Asn Thr Ser Glu Pro Gln His Leu Leu Val Met Lys Gly Ala		
500	505	510
Pro Glu Arg Ile Leu Asp Arg Cys Ser Ser Ile Leu Leu His Gly		
515	520	525
Lys Glu Gln Pro Leu Asp Glu Glu Leu Lys Asp Ala Phe Gln Asn		
530	535	540
Ala Tyr Leu Glu Leu Gly Gly Leu Gly Glu Arg Val Leu Gly Phe		
545	550	555
Cys His Leu Phe Leu Pro Asp Glu Gln Phe Pro Glu Gly Phe Gln		
560	565	570
Phe Asp Thr Asp Asp Val Asn Phe Pro Ile Asp Asn Leu Cys Phe		
575	580	585
Val Gly Leu Ile Ser Met Ile Asp Pro Pro Arg Ala Ala Val Pro		

590	595	600
Asp Ala Val Gly Lys Cys Arg Ser Aal Gly Ile Lys Val Ile Met		
605	610	615
Val Thr Gly Asp His Pro Ile Thr Ala Lys Ala Ile Ala Lys Gly		
620	625	630
Val Gly Ile Ile Ser Glu Gly Asn Glu Thr Val Glu Asp Ile Ala		
635	640	645
Ala Arg Leu Asn Ile Pro Val Ser Gln Val Asn Pro Arg Asp Ala		
650	655	660
Lys Ala Cys Val Val His Gly Ser Asp Leu Lys Asp Met Thr Ser		
665	670	675
Glu Gln Leu Asp Asp Ile Leu Lys Tyr His Thr Glu Ile Val Phe		
680	685	690
Ala Arg Thr Ser Pro Gln Gln Lys Leu Ile Ile Val Glu Gly Cys		
695	700	705
Gln Arg Gln Gly Ala Ile Val Ala Val Thr Gly Asp Gly Val Asn		
710	715	720
Asp Ser Pro Ala Leu Lys Lys Ala Asp Ile Gly Val Ala Met Gly		
725	730	735
Ile Ala Gly Ser Asp Val Ser Lys Gln Ala Ala Asp Met Ile Leu		
740	745	750
Leu Asp Asp Asn Phe Ala Ser Ile Val Thr Gly Val Glu Glu Gly		
755	760	765
Arg Leu Ile Phe Asp Asn Leu Lys Lys Ser Ile Ala Tyr Thr Leu		
770	775	780
Thr Ser Asn Ile Pro Glu Ile Thr Pro Phe Leu Ile Phe Ile Ile		
785	790	795
Ala Asn Ile Pro Leu Pro Leu Gly Thr Val Thr Ile Leu Cys Ile		
800	805	810
Asp Leu Gly Thr Asp Met Val Pro Ala Ile Ser Leu Ala Tyr Glu		
815	820	825
Gln Ala Glu Ser Asp Ile Met Lys Arg Gln Pro Arg Asn Pro Lys		
830	835	840
Thr Asp Lys Leu Val Asn Glu Arg Leu Ile Ser Met Ala Tyr Gly		
845	850	855
Gln Ile Gly Met Ile Gln Ala Leu Gly Gly Phe Phe Thr Tyr Phe		

860	865	870
Val Ile Leu Ala Glu Asn Gly Phe Leu Pro Ile His Leu Leu Gly		
875	880	885
Leu Arg Val Asp Trp Asp Asp Arg Trp Ile Asn Asp Val Glu Asp		
890	895	900
Ser Tyr Gly Gln Gln Trp Thr Tyr Glu Gln Arg Lys Ile Val Glu		
905	910	915
Phe Thr Cys His Thr Ala Phe Phe Val Ser Ile Val Val Val Gln		
920	925	930
Trp Ala Asp Leu Val Ile Cys Lys Thr Arg Arg Asn Ser Val Phe		
935	940	945
Gln Gln Gly Met Lys Asn Lys Ile Leu Ile Phe Gly Leu Phe Glu		
950	955	960
Glu Thr Ala Leu Ala Ala Phe Leu Ser Tyr Cys Pro Gly Met Gly		
965	970	975
Val Ala Leu Arg Met Tyr Pro Leu Lys Pro Thr Trp Trp Phe Cys		
980	985	990
Ala Phe Pro Tyr Ser Leu Leu Ile Phe Val Tyr Asp Glu Val Arg		
995	1000	1005
Lys Leu Ile Ile Arg Arg Arg Pro Gly Gly Trp Val Glu Lys Glu		
1010	1015	1020
Thr Tyr Tyr		

(2) INFORMATION FOR SEQ ID NO:7:

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 909 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GCC CGC GGG AAA GCC AAG GAG GAG GGC AGC TGG AAG AAA TTC	45		
Met Ala Arg Gly Lys Ala Lys Glu Glu Gly Ser Trp Lys Lys Phe			
1	5	10	15
ATC TGG AAC TCA GAG AAG GAG TTT CTG GGC AGG ACC GGT GGC	90		
Ile Trp Asn Ser Glu Lys Lys Glu Phe Leu Gly Arg Thr Gly Gly			
20	25	30	
AGT TGG TTT AAG ATC CTT CTA TTC TAC GTA ATA TTT TAT GGC TGC	135		
Ser Trp Phe Lys Ile Leu Leu Phe Tyr Val Ile Phe Tyr Gly Cys.			
35	40	45	

CTG GCT GGC ATC TTC ATC GGA ACC ATC CAA GTG ATG CTG CTC ACC		180
Leu Ala Gly Ile Phe Ile Gly Thr Ile Gln Val Met Leu Leu Thr		
50	55	60
ATC AGT GAA TTT AAG CCC ACA TAT CAG GAC CGA GTG GCC CCG CCA		225
Ile Ser Glu Phe Lys Pro Thr Tyr Gln Asp Arg Val Ala Pro Pro		
65	70	75
GGA TTA ACA CAG ATT CCT CAG ATC CAG AAG ACT GAA ATT TCC TTT		270
Gly Leu Thr Gln Ile Pro Gln Ile Gln Lys Thr Glu Ile Ser Phe		
80	85	90
CGT CCT AAT GAT CCC AAG AGC TAT GAG GCA TAT GTA CTG AAC ATA		315
Arg Pro Asn Asp Pro Lys Ser Tyr Glu Ala Tyr Val Leu Asn Ile		
95	100	105
GTT AGG TTC CTG GAA AAG TAC AAA GAT TCA GCC CAG AGG GAT GAC		360
Val Arg Phe Leu Glu Lys Tyr Lys Asp Ser Ala Gln Arg Asp Asp		
110	115	120
ATG ATT TTT GAA GAT TGT GGC GAT GTG CCC AGT GAA CCG AAA GAA		405
Met Ile Phe Glu Asp Cys Gly Asp Val Pro Ser Glu Pro Lys Glu		
125	130	135
CGA GGA GAC TTT AAT CAT GAA CGA GGA GAG CGA AAG GTC TGC AGA		450
Arg Gly Asp Phe Asn His Glu Arg Gly Glu Arg Lys Val Cys Arg		
140	145	150
TTC AAG CTT GAA TGG CTG GGA AAT TGC TCT GGA TTA AAT GAT GAA		495
Phy Lys Leu Glu Trp Leu Gly Asn Cys Ser Gly Leu Asn Asp Glu		
155	160	165
ACT TAT GGC TAC AAA GAG GGC AAA CCG TGC ATT ATT ATA AAG CTC		540
Thr Tyr Gly Tyr Lys Glu Gly Lys Pro Cys Ile Ile Ile Lys Leu		
170	175	180
AAC CGA GTT CTA GGC TTC AAA CCT AAG CCT CCC AAG AAT GAG TCC		585
Asn Arg Val Leu Gly Phe Lys Pro Lys Pro Pro Lys Asn Glu Ser		
185	190	195
TTG GAG ACT TAC CCA GTG ATG AAG TAT AAC CCA AAT GTC CTT CCC		630
Leu Glu Thr Tyr Pro Val Met Lys Tyr Asn Pro Asn Val Leu Pro		
200	205	210
GTT CAG TGC ACT GGC AAG CGA GAT GAA GAT AAG GAT AAA GTT GGA		675
Val Gln Cys Thr Gly Lys Arg Asp Glu Asp Lys Asp Lys Val Gly		
215	220	225
AAT GTG GAG TAT TTT GGA CTG GGC AAC TCC CCT GGT TTT CCT CTG		720
Asn Val Glu Tyr Phe Gly Leu Gly Asn Ser Pro Gly Phe Pro Leu		
230	235	240
CAG TAT TAT CCG TAC TAT GGC AAA CTC CTG CAG CCC AAA TAC CTG		765

Gln	Tyr	Tyr	Pro	Tyr	Tyr	Gly	Lys	Leu	Leu	Gln	Pro	Lys	Tyr	Leu	
								245	250					255	
CAG	CCC	CTG	CTG	GCC	GTA	CAG	TTC	ACC	AAT	CTT	ACC	ATG	GAC	ACT	810
Gln	Pro	Leu	Leu	Ala	Val	Gln	Phe	Thr	Asn	Leu	Thr	Met	Asp	Thr	
							260		265			270			
GAA	ATT	CGC	ATA	GAG	TGT	AAG	GCG	TAC	GGT	GAG	AAC	ATT	GGG	TAC	855
Glu	Ile	Arg	Ile	Glu	Cys	Lys	Ala	Tyr	Gly	Glu	Asn	Ile	Gly	Tyr	
						275		280			285				
AGT	GAG	AAA	GAC	CGT	TTT	CAG	GGA	CGT	TTT	GAT	GTA	AAA	ATT	GAA	900
Ser	Glu	Lys	Asp	Arg	Phe	Gln	Gly	Arg	Phe	Asp	Val	Lys	Ile	Glu	
						290		295			300				
GTT	AAG	AGC													909
Val	Lys	Ser													

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Ala	Arg	Gly	Lys	Ala	Lys	Glu	Glu	Gly	Ser	Trp	Lys	Lys	Phe	
1					5				10				15		
Ile	Trp	Asn	Ser	Glu	Lys	Lys	Glu	Phe	Leu	Gly	Arg	Thr	Gly	Gly	
					20				25				30		
Ser	Trp	Phe	Lys	Ile	Leu	Leu	Phe	Tyr	Val	Ile	Phe	Tyr	Gly	Cys	
					35				40				45		
Leu	Ala	Gly	Ile	Phe	Ile	Gly	Thr	Ile	Gln	Val	Met	Leu	Leu	Thr	
					50				55				60		
Ile	Ser	Glu	Phe	Lys	Pro	Thr	Tyr	Gln	Asp	Arg	Val	Ala	Pro	Pro	
					65				70				75		
Gly	Leu	Thr	Gln	Ile	Pro	Gln	Ile	Gln	Lys	Thr	Glu	Ile	Ser	Phe	
					80				85				90		
Arg	Pro	Asn	Asp	Pro	Lys	Ser	Tyr	Glu	Ala	Tyr	Val	Leu	Asn	Ile	
					95				100				105		
Val	Arg	Phe	Leu	Glu	Lys	Tyr	Lys	Asp	Ser	Ala	Gln	Arg	Asp	Asp	
					110				115				120		
Met	Ile	Phe	Glu	Asp	Cys	Gly	Asp	Val	Pro	Ser	Glu	Pro	Lys	Glu	
					125					130			135		
Arg	Gly	Asp	Phe	Asn	His	Glu	Arg	Gly	Glu	Arg	Lys	Val	Cys	Arg	

140	145	150
Phy Lys Leu Glu Trp Leu Gly Ash Cys Ser Gly Leu Asn Asp Glu		
155	160	165
Thr Tyr Gly Tyr Lys Glu Gly Lys Pro Cys Ile Ile Ile Lys Leu		
170	175	180
Asn Arg Val Leu Gly Phe Lys Pro Lys Pro Pro Lys Asn Glu Ser		
185	190	195
Leu Glu Thr Tyr Pro Val Met Lys Tyr Asn Pro Asn Val Leu Pro		
200	205	210
Val Gln Cys Thr Gly Lys Arg Asp Glu Asp Lys Asp Lys Val Gly		
215	220	225
Asn Val Glu Tyr Phe Gly Leu Gly Asn Ser Pro Gly Phe Pro Leu		
230	235	240
Gln Tyr Tyr Pro Tyr Tyr Gly Lys Leu Leu Gln Pro Lys Tyr Leu		
245	250	255
Gln Pro Leu Leu Ala Val Gln Phe Thr Asn Leu Thr Met Asp Thr		
260	265	270
Glu Ile Arg Ile Glu Cys Lys Ala Tyr Gly Glu Asn Ile Gly Tyr		
275	280	285
Ser Glu Lys Asp Arg Phe Gln Gly Arg Phe Asp Val Lys Ile Glu		
290	295	300
Val Lys Ser		

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGGGGAAGG GGGTTGGACG TGAT 24

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATAGTAGGTT TCCTTCTCCA CCCA 24

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGGCCCGCG GGAAAGCCAA GGAG 24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCTCTTAACT TCAATTTTA CATC 24